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## Exhibit A

### Pairwise Alignment

Sequence 1: Fig.11A 5393670

Sequence 2: SEQIDNO1 09/888,224

Optimal Global alignment

Alignment score: -1036

Identities: 0.34

Fig.11A 5393670 1 ----- 1  
SEQIDNO1 09/888,224 1 atgataaacgttgcaacgggagaggagacccaatacacctctttggagtcaactgggttc 60

Fig.11A 5393670 1 ----- 1  
SEQIDNO1 09/888,224 61 ggctttgagacaccgaactacgttggttcacggcctatggagttaggaactgggaggacatg 120

Fig.11A 5393670 1 ----- 1  
SEQIDNO1 09/888,224 121 ctctccagatcaagagccttggttcaatgcgataagggttccttctgtacccagtca 180

Fig.11A 5393670 1 ----- 1  
SEQIDNO1 09/888,224 181 gtaaaaccggggacgatgccaacggcgattgactacgccaagaaccagacctccagggt 240

Fig.11A 5393670 1 ----- 1  
SEQIDNO1 09/888,224 241 cttgacagcgtccagataatggagaaaataatcaagaaggctggagacctgggcatattc 300

Fig.11A 5393670 1 ----- 29  
SEQIDNO1 09/888,224 301 gtgctccctcgaacacacagaaatggggaacacttataagaacccctatggtacacggac 360

Fig.11A 5393670 30 TGGC-GTT-CACTACGG-CAI-----CTGACC---A-TTC-CC-CCCTCTCGC- 72  
SEQIDNO1 09/888,224 361 agcttctcggagcgggaactacataaacagcttggttgagtccgcagagctccggcaag 420

Fig.11A 5393670 72 --C-CCCG--A-----GCA-A-CC---G---CTA---C-CA---C-CCCCCG---A 102  
SEQIDNO1 09/888,224 421 taatggaaggttctcggcggggacttaaaacgaacccacactctgaagccccacact 480

Fig.11A 5393670 103 G---C-----T-CC-A-TC---CGAGTTAC-BA---CTTACAGT-----G---TAC 135  
SEQIDNO1 09/888,224 481 gccctctacacgaagggaagtgggggacatgggggaatggggaatgacgccaccgaactgg 540

Fig.11A 5393670 136 A-----ATTCTC-AGCGGCGC---TTC-----CCCACTA--GAGTTGGT-GGTCC-- 176  
SEQIDNO1 09/888,224 541 aacctggcggttaaaacataggaaggaacattctgggaacttgcccaataatgggtata 600

Fig.11A 5393670 176 ---TTGACTTG---A-----ACTT-CCGTCCAGGCACTAC--G---G-AA---AGTAC 214  
SEQIDNO1 09/888,224 601 tttgttgagggaaccccggttcacaccccgagaaagacgtaggtataagtgggggccac 660

Fig.11A 5393670 215 A---CCTCTTCACTTC-AAI-----CCCGG-----CG-TCCA-----C--- 244  
SEQIDNO1 09/888,224 661 gacgcctggttgggggaacacattatgggtgttataaataccacgttaacctgcccagg 720

Fig.11A 5393670 244 -ACCC-CC---CC-TCT-----C-----C-----TGAAGAG-----C 267  
SEQIDNO1 09/888,224 721 gacaggttattttataaccccaagtttatgggttagaagtttacgacacccctacttt 780

Fig.11A 5393670 268 G---G-----TG-TG---G-CAG-----GAC-C-TCCTATCG-----GGG--C 298  
SEQIDNO1 09/888,224 781 gacccgggtgagggttcccccaacacctccccgaattatggaacacacttccgactac 840

Fig.11A 5393670 299 GTCG-AA-T-A-----C-A-----CC-----GCC-T-C-CCGTGC-ACCAAT-T 329  
SEQIDNO1 09/888,224 841 gaaagtggtctgtgttaccctgtgttataggttagtcgaaggaagtaacggacat 900

Fig.11A 5393670 330 CACTC-----CAGCC---TCACCA---TAAACCA-----TTC-----ATGCCAGG 367  
SEQIDNO1 09/888,224 901 ggttggaacccggggatgtaattggcactacataataataggtggatgacacgaac 960

Fig.11A 5393670 368 AG---CTCTGCGG---CTAC---AGTAACGTCT---CTCT---T-----CTCTTA-T 406  
SEQIDNO1 09/888,224 961 aaatttggaattcttctatgggaattgaacccaacagggtgacacactggaact 1020

Fig.11A 5393670 407 CTCCT---GAGCT---A-----C-CT-TT---ATTAAGTGCTGCT---T---GCTTA-- 446  
SEQIDNO1 09/888,224 1021 ctgaagatgaaggacacaaattgggaagacaaatgaacacactgaagggtgactg 1080

Fig.11A 5393670 446 -ATGG---CAAGGCTTA-GCTTGACCT-CAACTTCTTGT---TTC-----G- 487  
SEQIDNO1 09/888,224 1081 gaaagtggttcttaaacuccaactggccctccctcccaagaaatgacaacaacaagc 1140

Fig.11A 5393670 487 ---CCCT-----GIG---GA---GA---GA---AGCGT-----GGT 510  
SEQIDNO1 09/888,224 1141 acaccuccaacgaccacaacgaacacacatccactccacgacacacaccagaccag 1200

Fig.11A 5393670 510 -GTATG-TGTCTAG---TGACG---GA---ACGGGGG---CC---AA---CCA 549  
SEQIDNO1 09/888,224 1201 accatgactatgcaactacaaaccccaaccacacacacacacacacacacacacac 1260

Fig.11A 5393670 549 ---G---TA-TAA---SAGGCGTGGCACTAA---GGG---A---SCGGC 584  
SEQIDNO1 09/888,224 1261 tttaaaatgtgacgttctctcgaactauctctcngttagaggaaccgcgtgaggtt 1320

Fig.11A 5393670 585 AC-TGCCAT-CTCAGTCCCGTCCAG-ACAT---G---A---AC---GCGCC 628  
SEQIDNO1 09/888,224 1321 gtatgtatgaaaccagctctgca-tccagcgttgggagctccgaacctctgaggt 1379

Fig.11A 5393670 629 C-----TC-----AA--G-AF-TACCAACCGGGCTCT-CTCTCAACAGAGTGA-TA 671  
SEQIDNO1 09/888,224 1380 gtttaaaatgggaa-cgcacaggaacccacacttagggctctggggagcgtttca 1439

Fig.11A 5393670 672 TCCTGG-----AGGGCAACTCG--G---GGG---AATTC---CTT--G-ACC-----G- 707  
SEQIDNO1 09/888,224 1440 gattccaccccaagacattggaicccacacacaaaagttagaga-aaggaaaggggtgt 1499

Fig.11A 5393670 708 C-----TC-----GCTCTTCAAGGCCAG-GGGCTG---G-----ACTCT- 741  
SEQIDNO1 09/888,224 1500 caaggttataacctctgaaatcagatgacacgaatataacacaaagccatacc 1559

Fig.11A 5393670 742 C--GG---TTGCGCTTCAACCCCTATCC---CA-G---GGCTAC-AFA-----A 779  
SEQIDNO1 09/888,224 1560 ggaggtcatalacagggcaggtctgggcaacagcgaataaacgctcagacttcgt 1619

Fig.11A 5393670 780 GCT-AT--T--AC---GCCCCG--GATAG-GCTT-----G-ACAG-CTC-- 813  
SEQIDNO1 09/888,224 1620 gctccgataaagttctcccaacttcagggatctcagacacaaagtcaggtga 1679

Fig.11A 5393670 814 CAAGACCTT-----GCAATGATC-----ACT---CAGTTC-----CACGGA 849  
SEQIDNO1 09/888,224 1680 aagaggttcccgggaaagaaatggccttgagggttggtctcaagggtgcacaa 1739

Fig.11A 5393670 850 CAC--GG-TG---GCCCTCG--CA--C-CTT-GAGCATGACCGGAATACCA 897  
SEQIDNO1 09/888,224 1740 cttgaggtgacaggtcaggtactacgggtaaagaaacagctctacatgaggggg 1799

Fig.11A 5393670 898 GCA--AA--GGGTGAG--TCCCAACCGCCGCGCCGCG---GAC-C---CC- 943  
SEQIDNO1 09/888,224 1800 ctctcttggtggtatagaaagggggcattttctcaggttatcttccatattcggtga 1859

Fig.11A 5393670 943 ---A---TCI---G-TT-----GCGCCCTCCGCT---G--A-KCTAC-GCC 977  
SEQIDNO1 09/888,224 1860 tggagggttgaaacaaattttgaggtctaaagttatagagggttcgggatga 1919

Fig.11A 5393670 978 C-----G---TCCTGCT---GTGGG---G---C-----TGA-- 1005  
SEQIDNO1 09/888,224 1920 cttcttcaccttaaaagaaatgaagtaactaacggttagaggttggtcttactacac 1979

Fig.11A 5393670 1005 ---GGC-GC---ATG---GCTTTGT-T---GAGATTGGAAGGAGAG 1047  
SEQIDNO1 09/888,224 1980 caaatctataaaatagttacaacacagcggcggtggtctcacacacactact 2039

Fig.11A 5393670 1048 CCAGTAAT-CTT-----GTTT-----GTGGCACT-CTAGG-----CGAG--G 1085  
SEQIDNO1 09/888,224 2040 gatctcctggaattcgggttcgaatataacacaggttctctcattccatagac 2099

Fig.11A 5393670 1086 C-----G---GAGC-ACC---GATGCA-----GCTCCAC----- 1118  
SEQIDNO1 09/888,224 2100 agtggagtaagggtggtcttgaaagtacattctcctggcggggaacattggc 2159

Fig.11A 5393670 1119 TCG-----G---AA-----G-----G---CAAG 1138  
SEQIDNO1 09/888,224 2160 cactgaggagacatgaggttctcgtggaggggtccggcctccgcttcataaac 2219

Fig.11A 5393670 1139 A-TG---ACTTGT-T-----GTCACATGCGGGGGAGATTGGGT-AG 1185  
SEQIDNO1 09/888,224 2220 attcagagaaatatacaaccacaacacagcgaataccactatcacactagac 2279

Fig.11A 5393670 1186 TAGGAATTGGAGGGGCGCTCGCTCTGTTGGTGGAGAG-ATTTCAG----- 1239  
SEQIDNO1 09/888,224 2280 tttaaccacacaaagaaactacaggtgaaacacaggaactctcagaggtaat 2339

Fig.11A 5393670 1240 TACAGGAG--GCTCCTCTCTCGACACACCTGACGCAAT-TCATTGGG 1297  
SEQIDNO1 09/888,224 2340 taggtcaggtcccggaactggggcattggccaaagcccaattacagggagga 2399

Fig.11A 5393670 1298 CATTG---CT---GG-CAATGG-ACG---G---GTG---G---G---GT 1340  
SEQIDNO1 09/888,224 2400 ggaaccacaaatctctatataaaatgaacattgaagtctatgggctaaaggt 2459

Fig.11A 5393670 1341 GGGC-C-T-AGGTCGCTATGAA-A-TACTAT---ACT-TC-TA-TGCT---TAG 1390

SEQIDNO1 09/888,224 2460 caccgagaggaacaaacatgagaggggtctccactaccacagggccctggatag 2519

Fig.11A 5393670 1391 AGCGTGACT 1400

SEQIDNO1 09/888,224 2520 tataatgatga 2529

Fig.11A 5393670 1 ----- 1  
SEQIDNO1 09/888,224 1 MINVATGEETPIHLFGVNWFGFETPNYVVHGLWSRNWEDMLLQIKSLGFNAIRLPFCTQS 60

Fig.11A 5393670 1 -----XXXP-XXW-X-XXXXXX 15  
SEQIDNO1 09/888,224 61 VKPGTMPTAIDYAKNPDLQGLDSVQIMEKIIKKAGDLGIFVLLDYHRIGCNFIEPIWYTD 120

Fig.11A 5393670 16 CXXDHGXX-XXXXXXXXLVXXXP-X-XXPX-V-XXXTXXXX-XXXXXXXXKLXXXYKX-XY 68  
SEQIDNO1 09/888,224 121 SFSEQDYINTVEVAQRFGKYWNVIGDLKNEPHSSSAPAAAYTDGSGATWGMGNATDW 180

Fig.11A 5393670 69 X-XXSGVXXX-XQXXRX-X-XDW-X-XXRWMHDXXX-XYXXSCTVXX--XR-XXQ-X- 116  
SEQIDNO1 09/888,224 181 NLAAERIGRAILEVAQWIFVEGTQFTPEIDGRYKWHNAWWGGNLMGVRKYPVNLPR 240

Fig.11A 5393670 117 XH-XXX-X-X-X-XXEX-XXX--XX-XX--XXCFIX-XXXXXXXX-X---AXXVVDX 158  
SEQIDNO1 09/888,224 241 DKVVYSPQVYGSEVYQPYFDPGEGFPDNLPEIWHYHFFYKLDLGYPVVIGEFCKYGH 300

Fig.11A 5393670 159 RAXSXXIXXQ--Y--MPSXXSGXX--SVVXX-X-XXIXXIX-XXXXXVMMXXIX 211  
SEQIDNO1 09/888,224 301 GGDPRDVWQKIIDWMIQNKCFDFWNNPNNGDTGIGKDWTTIWEDKNNKRM 360

Fig.11A 5393670 212 XG-XXAXASTXDLXS--X-XX---XXXXXXXXA--XAXXSQXWIXXIGA--X-X- 256  
SEQIDNO1 09/888,224 361 DSCSNATAPSVPTTTTTTSTPTTTTTTSTPTTTQTPTTTPTTTTTPSNNV 420

Fig.11A 5393670 256 -XXXX-XTAGAN--X-AAXXXXXPVXXXX-XXXTX-XXXXXXSHGFXLQDQX 309  
SEQIDNO1 09/888,224 421 FEIVNVLPTSSQVETSVEVVGITGAXRLGSSEPLSR\*NRKRHHGPRLGGRLQ 480

Fig.11A 5393670 310 SW-XQLXXXX-NXXXXX-XX-XXXIARPX-C-X-XXS-XXX-LPLPW-XX--GYXXX 358  
SEQIDNO1 09/888,224 481 DCTPHWNRQHKDGDKERGAQGYKPEHQHSEV\*HNGIPGGHIERALGQPANKRSELR 540

Fig.11A 5393670 359 XXXX--PXIXX-X-XXQD---HHHX-XXXVXX-HGQXIXXIX-XXXCEHHPQVP 408  
SEQIDNO1 09/888,224 541 APDKGLPSEIT\*HKVARKEPGKQLRL\*GLALQGCQHEITRGGLRDNGTALHRGR 600

Fig.11A 5393670 409 AXNXRXXPAAQPGXX-X-X-X-S-XV--XAPPPXXXLKAX--XLAT-XGXXX-XXX-- 456  
SEQIDNO1 09/888,224 601 LSCGLQGA\*SHR\*CSNRRWKACKPDF\*ALRHSGCRMVHLQAN\*ELRLRGCVRLH 660

Fig.11A 5393670 456 --QXXW-XAXXHLRQQPXX-XXX-LDSXQX-XRXX-X-XQXX-EGX--IQX- 504  
SEQIDNO1 09/888,224 661 QIHNS\*QLP\*RWPHPLPD\*PGIRYRDIHQRVHLIPMHSGRKVDP\*QVQVHPGERNNG 720

Fig.11A 5393670 505 SX-XX-X--XX-X---PXXXXVXX--XSIRWGDIGXYELDCAPAPCVQHDXFRX- 552  
SEQIDNO1 09/888,224 721 H\*GHSSRRRGPPASRFHNIADDFNHNPAHYHYD\*DFNHHYNHLT\*DNHRTCSGRN 780

Fig.11A 5393670 553 YTEXARLRAAARRXHGQX-XXXWXTXXVXXXXXXRXAXXVPV\*XTTXXXQCE-\* 610  
SEQIDNO1 09/888,224 781 \*AQVPGWAV\*GPN\*QGRRKPRVL\*RNKPVEHTER\*KLRRDDLQLE\*RGSPLRPG\* 840

Fig.11A 5393670 611 SVD 613  
SEQIDNO1 09/888,224 841 YMM 843